

**Table S2: Z-score for protein disorder abundance for disorder regions > 30 residues**

Organism <sup>a</sup>	">%long30" <sup>b</sup>		
	MD <sup>c</sup>	IUPred <sup>c</sup>	NORSnet <sup>c</sup>
<b>Thermophiles</b>			
<i>Thermosynechococcus elongatus</i> BP-1	-0.5	-0.4	0.3
<i>Clostridium clariflavum</i> DSM 19732	-0.5	-0.9	-0.9
<i>Streptococcus thermophilus</i> LMG 18311	0.2	-0.5	-0.3
<b>Hyperthermophiles</b>			
<i>Aeropyrum pernix</i> K1	-1.2	-0.8	-1.0
<i>Pyrococcus horikoshii</i> OT3	-1.4	-1.1	0.7
<b>Psychrophiles</b>			
<i>Desulfotalea psychrophila</i> LSv54	-0.6	-0.7	-0.5
<i>Colwellia psychrerythraea</i> 34H	-0.3	-0.7	-0.6
<i>Shewanella woodyi</i> ATCC 51908	-0.8	-0.6	-0.3
<b>Psychrotolerants</b>			
<i>Methanococcoides burtonii</i> DSM 6242	-1.1	-0.7	-0.7
<i>Leuconostoc citreum</i> KM20	-0.1	-0.4	-0.5
<i>Bacillus weihenstephanensis</i> KBAB4	-0.2	-0.5	-0.7
<i>Rhodoferax ferrireducens</i> T118	-0.7	-0.2	0.0
<b>Halophiles</b>			
<i>Haloarcula marismortui</i> ATCC 43049	1.7	3.6	1.0
<i>Halobacterium</i> sp. NRC-1	1.4	3.0	0.3
<i>Marinobacter aquaeolei</i> VT8	-0.1	0.4	0.2
<b>Alkalophile</b>			
<i>Bacillus halodurans</i> C-125	-0.3	-0.3	-0.7
<b>Radiation resistant</b>			
<i>Deinococcus deserti</i> VCD115	-0.8	0.7	1.0
<i>Deinococcus maricopensis</i> DSM 21211	-1.1	0.7	0.2
<i>Deinococcus radiodurans</i>	-0.1	1.7	-0.7
<b>Taxonomic neighbors (mesophiles)</b>			
<i>Caulobacter vibrioides</i>	0.3	0.7	1.4
<i>Chromobacterium violaceum</i> ATCC 12472	-0.4	0.0	0.4
<i>Clostridium acetobutylicum</i>	-0.3	-0.6	0.0
<i>Corynebacterium glutamicum</i>	0.4	0.8	1.3
<i>Desulfovibrio vulgaris</i> str. Hildenborough	0.9	1.1	0.6

<i>Geobacter metallireducens</i> GS-15	-0.6	-0.2	-0.1
<i>Geobacter sulfurreducens</i> PCA	-0.4	-0.1	0.2
<i>Lactococcus lactis</i> subsp. <i>lactis</i> II1403	0.4	-0.4	-0.3
<i>Listeria innocua</i>	0.1	-0.4	-0.7
<i>Methanosa</i> cina mazei Go1	-0.1	-0.1	0.0
<i>Methanococcus maripaludis</i> S2	-0.7	-1.0	-1.0
<i>Nitrosomonas europaea</i> ATCC 19718	-0.2	-0.2	-0.1
<i>Pseudoalteromonas atlantica</i> T6c	-0.9	-0.3	-0.3
<i>Rhodopseudomonas palustris</i> CGA009	0.1	0.6	1.0
<i>Rhodospirillum rubrum</i> ATCC 11170	-0.1	0.5	0.6
<i>Rhodobacter sphaeroides</i> 2.4.1	-0.1	0.4	0.3
<i>Shewanella oneidensis</i>	0.3	-0.6	-0.3
<i>Ruegeria pomeroyi</i> DSS-3	-1.3	-0.2	-0.5
<i>Streptomyces coelicolor</i>	1.0	3.3	2.8
<i>Synechococcus elongatus</i> PCC 6301	-0.4	-0.3	0.7
<i>Synechocystis</i> sp. PCC 6803 substr. Kazusa	0.1	-0.2	0.4

- a. Organism marks the full name of the organism where grey cells correspond to the environments; Taxonomic neighbors correspond to organisms that are related in phylogeny to the extremophiles described in this study. We compiled averages (ave) and standard deviations (sd) over a set of 1,613 complete prokaryotic proteomes taken from UniProt. Eukaryotes are not included due the difference in disorder content ( $MD_{ave}=14.6\%$ ,  $MD_{sd}=4.2\%$ ;  $NORsnet_{ave}=2.5\%$ ,  $NORsnet_{sd}=2.0\%$ ;  $IUPred_{ave}=7.5\%$  and  $IUPred_{sd}=5.5\%$ ).
- b. Disorder %long30 refers to the percentage of proteins in a proteome that contains at least one region with  $\geq 30$  consecutive residues predicted as disordered.
- c.  $\langle MD | IUPred | NORsnet \rangle$  refer to the three prediction methods used, in order to catch the different “flavors” of disorder.